

## SEQUENCE LISTING

<110> JONES, DAVID  
MANOS, ELIZABETH

<120> TRDL-1 gamma, A NOVEL TUMOR NECROSIS-LIKE LIGAND

<130> 1321.2.34

<150> 60/157,913

<151> 1999-10-06

<160> 5

<170> PatentIn version 3.0

<210> 1

<211> 1607

<212> DNA

<213> Homo sapiens

<400> 1

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&lt;210&gt; 2

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Gly  
1 5 10 15Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu  
Trp  
20 25 30Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala  
Leu  
35 40 45Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser  
Arg  
50 55 60Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro  
Trp  
65 70 75  
80Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu  
Asn

85

90

95

Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln  
Lys

100

105

110

Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser  
Lys

115

120

125

Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg  
Arg

130

135

140

Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp  
Ala  
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160

150

155

Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr  
Phe

165

170

175

Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu  
Thr

180

185

190

Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala  
Tyr

195

200

205

Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp  
Ile

210

215

220

Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser  
Pro  
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230

235

240

His Gly Thr Phe Leu Gly Leu  
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Trp  
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Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala  
Leu  
35 40 45

Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser  
Arg  
50 55 60

Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro

Trp															
65															
80															
Gln	Ser	Leu	Pro	Glu	Gln	Ser	Ser	Asp	Ala	Leu	Glu	Ala	Trp	Glu	
Asn															
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Gly	Glu	Arg	Ser	Arg	Lys	Arg	Arg	Ala	Val	Leu	Thr	Gln	Lys	Gln	
Lys															
			100					105					110		
Lys	Gln	His	Ser	Val	Leu	His	Leu	Val	Pro	Ile	Asn	Ala	Thr	Ser	
Lys															
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Asp	Asp	Ser	Asp	Val	Thr	Glu	Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	
Arg															
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Gly	Arg	Gly	Leu	Gln	Ala	Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	
Ala															
145					150					155					
160															
Gly	Val	Tyr	Leu	Leu	Tyr	Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	
Phe															
			165						170					175	
Thr	Met	Gly	Gln	Val	Val	Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	
Thr															
			180						185				190		
Leu	Phe	Arg	Cys	Ile	Arg	Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	
Tyr															
		195					200					205			
Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	
Ile															

210

215

220

Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser  
 Pro  
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His Gly Thr Phe Leu Gly Phe Val Lys Leu  
 245 250

<210> 5  
 <211> 234  
 <212> PRT  
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<400> 5

Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro  
 Gly  
 1 5 10 15

Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu  
 Trp  
 20 25 30

Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala  
 Leu  
 35 40 45

Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser  
 Arg  
 50 55 60

Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro  
 Trp  
 65 70 75  
 80

Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu  
 Asn  
 85 90 95

Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln  
Lys

100

105

110

Asn Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg  
Arg

115

120

125

Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp  
Ala

130

135

140

Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr  
Phe

145

150

155

160

Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu  
Thr

165

170

175

Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala  
Tyr

180

185

190

Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp  
Ile

195

200

205

Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser  
Pro

210

215

220

His Gly Thr Phe Leu Gly Phe Val Lys Leu  
225 230